

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 4, 2003, 17:37:38 ; Search time 19 Seconds

(without alignments)
38.406 Million cell updates/sec

Title: US-09-865-548a-13

Perfect score: 43

Sequence: 1 GLEKNIEL 9

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 405691 seqs, 81078759 residues

Total number of hits satisfying chosen parameters: 405691

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents, AA, New:*
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3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	582	US-09-724-676-93768	Sequence 93768, A
2	43	100.0	582	US-09-724-676-93768	Sequence 93768, A
3	43	100.0	587	US-09-724-676-93776	Sequence 93776, A
4	43	100.0	587	US-09-724-676-93776	Sequence 93776, A
5	43	100.0	594	US-09-724-676-93784	Sequence 93784, A
6	43	100.0	594	US-09-724-676-93784	Sequence 93784, A
7	43	100.0	937	US-09-724-676-93767	Sequence 93767, A
8	43	100.0	937	US-09-724-676-93767	Sequence 93767, A
9	43	100.0	942	US-09-724-676-93775	Sequence 93775, A
10	43	100.0	942	US-09-724-676-93775	Sequence 93775, A
11	43	100.0	949	US-09-724-676-93783	Sequence 93783, A
12	43	100.0	949	US-09-724-676-93783	Sequence 93783, A
13	43	100.0	1404	US-09-724-676-93766	Sequence 93766, A
14	43	100.0	1404	US-09-724-676-93766	Sequence 93766, A
15	43	100.0	1409	US-09-724-676-93773	Sequence 93773, A
16	43	100.0	1409	US-09-724-676-93773	Sequence 93773, A
17	43	100.0	1416	US-09-724-676-93782	Sequence 93782, A
18	43	100.0	1416	US-09-724-676-93782	Sequence 93782, A
19	43	100.0	1587	US-09-724-676-93765	Sequence 93765, A
20	43	100.0	1587	US-09-724-676-93765	Sequence 93765, A
21	43	100.0	1591	US-09-724-676-93764	Sequence 93764, A
22	43	100.0	1591	US-09-724-676-93764	Sequence 93764, A
23	43	100.0	1592	US-09-724-676-93772	Sequence 93772, A
24	43	100.0	1592	US-09-724-676-93772	Sequence 93772, A
25	43	100.0	1596	US-09-724-676-93771	Sequence 93771, A
26	43	100.0	1596	US-09-724-676-93771	Sequence 93771, A

27	43	100.0	1599	US-09-724-676-93781	Sequence 93781, A
28	43	100.0	1599	US-09-724-676-93781	Sequence 93781, A
29	43	100.0	1603	US-09-724-676-93780	Sequence 93780, A
30	43	100.0	1603	US-09-724-676-93780	Sequence 93780, A
31	43	100.0	1604	US-09-724-676-93786	Sequence 93786, A
32	43	100.0	1604	US-09-724-676-93786	Sequence 93786, A
33	43	100.0	1609	US-09-724-676-93770	Sequence 93770, A
34	43	100.0	1609	US-09-724-676-93770	Sequence 93770, A
35	34	79.1	232	US-09-134-000C-3684	Sequence 3684, A
36	34	79.1	232	US-09-134-000C-3684	Sequence 3684, A
37	34	79.1	384	US-10-289-757-119	Sequence 119, App
38	34	79.1	398	US-10-289-757-186	Sequence 186, App
39	33	76.7	974	PCT-US02-16164-106	Sequence 106, App
40	32	74.4	122	US-10-092-411A-3014	Sequence 3014, App
41	31	72.1	106	US-09-513-999C-5448	Sequence 5448, App
42	31	72.1	130	US-09-724-676-70251	Sequence 70251, A
43	31	72.1	130	US-09-724-676-70251	Sequence 70251, A
44	31	72.1	136	US-09-724-676-28858	Sequence 28858, A
45	31	72.1	136	US-10-057-498-28858	Sequence 28858, A

ALIGNMENTS

RESULT 1
US-09-724-676-93768
; Sequence 93768, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724, 676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93768
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-93768

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Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLEKNIEL 9
DB 413 GLEKNIEL 421

RESULT 2
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; Sequence 93768, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: CompuGen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 CompuGen
; CURRENT APPLICATION NUMBER: US/09/724, 676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93768
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-93768

Query Match 100.0%; Score 43; DB 5; Length 582;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLEKNIEL 9
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-93767

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Best Local Similarity 100.0%; Score 43; DB 5; Length 937;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLIEKNIEL 9
DB 413 GLIEKNIEL 421

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US-09-724-676-93775
; Sequence 93775, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93775
; LENGTH: 942
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-93775

Query Match
Best Local Similarity 100.0%; Score 43; DB 5; Length 942;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLIEKNIEL 9
DB 418 GLIEKNIEL 426

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US-09-724-676A-93775
; Sequence 93775, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93775
; LENGTH: 942
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-93775

Query Match
Best Local Similarity 100.0%; Score 43; DB 5; Length 942;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLIEKNIEL 9
DB 418 GLIEKNIEL 426

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US-09-724-676-93783
; Sequence 93783, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
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; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93783
; LENGTH: 949
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-93783

Query Match
Best Local Similarity 100.0%; Score 43; DB 5; Length 949;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLIEKNIEL 9
DB 425 GLIEKNIEL 433

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US-09-724-676A-93783
; Sequence 93783, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93783
; LENGTH: 949
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-93783

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLIEKNIEL 9
DB 425 GLIEKNIEL 433

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; Sequence 93766, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93766
; LENGTH: 1404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-93766

Query Match
Best Local Similarity 100.0%; Score 43; DB 5; Length 1404;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLIEKNIEL 9
DB 413 GLIEKNIEL 421

RESULT 14
US-09-724-676A-93766
; Sequence 93766, Application US/09724676A
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GenCore version 5.1.3
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Run on: February 4, 2003, 17:36:58 ; Search time 139 Seconds

(without alignments)
41.745 Million cell updates/sec

Title: US-09-865-548A-13

Perfect score: 43

Sequence: 1 GLEKNIETL 9

Scoring table: BLOSUM62

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	43	100.0	161	21	US-09-758-442-394
4	43	100.0	161	26	US-10-217-623-394
5	43	100.0	1042	1	PCT-US01-08631-44754
6	43	100.0	1080	1	PCT-US01-08631-44755

7	43	100.0	1280	27	US-60-389-987-2114	Sequence 2114, App
8	43	100.0	1280	27 <th>US-60-412-418-2114</th> <th>Sequence 2114, App</th>	US-60-412-418-2114	Sequence 2114, App
9	43	100.0	1603	18 <th>US-09-488-725A-3447</th> <th>Sequence 3447, App</th>	US-09-488-725A-3447	Sequence 3447, App
10	43	100.0	1616	19 <th>US-09-538-092-1016</th> <th>Sequence 1016, App</th>	US-09-538-092-1016	Sequence 1016, App
11	43	100.0	1687	27 <th>US-60-258-278-16</th> <th>Sequence 16, App</th>	US-60-258-278-16	Sequence 16, App
12	43	100.0	1695	27 <th>US-60-245-227-60</th> <th>Sequence 60, App</th>	US-60-245-227-60	Sequence 60, App
13	42	97.7	1568	25 <th>US-10-155-881-27185</th> <th>Sequence 27185, A</th>	US-10-155-881-27185	Sequence 27185, A
14	35	81.4	269	20 <th>US-09-614-150-30279</th> <th>Sequence 30279, A</th>	US-09-614-150-30279	Sequence 30279, A
15	35	81.4	269	27 <th>US-60-191-637-29827</th> <th>Sequence 29827, A</th>	US-60-191-637-29827	Sequence 29827, A
16	35	81.4	323	27 <th>US-60-150-582-475</th> <th>Sequence 475, App</th>	US-60-150-582-475	Sequence 475, App
17	35	81.4	425	27 <th>US-60-361-742-892</th> <th>Sequence 892, App</th>	US-60-361-742-892	Sequence 892, App
18	34	79.1	183	26 <th>US-10-219-999-38244</th> <th>Sequence 38244, A</th>	US-10-219-999-38244	Sequence 38244, A
19	34	79.1	183	27 <th>US-60-312-544-7998</th> <th>Sequence 7998, App</th>	US-60-312-544-7998	Sequence 7998, App
20	34	79.1	190	25 <th>US-10-138-145-896</th> <th>Sequence 896, App</th>	US-10-138-145-896	Sequence 896, App
21	34	79.1	232	15 <th>US-09-134-000-3684</th> <th>Sequence 3684, App</th>	US-09-134-000-3684	Sequence 3684, App
22	34	79.1	232	21 <th>US-09-791-537-114254</th> <th>Sequence 114254, A</th>	US-09-791-537-114254	Sequence 114254, A
23	34	79.1	254	1 <th>PCT-US02-03987-10730</th> <th>Sequence 10730, A</th>	PCT-US02-03987-10730	Sequence 10730, A
24	34	79.1	254	22 <th>US-09-815-242-10730</th> <th>Sequence 10730, A</th>	US-09-815-242-10730	Sequence 10730, A
25	34	79.1	254	24 <th>US-10-072-851-10730</th> <th>Sequence 10730, A</th>	US-10-072-851-10730	Sequence 10730, A
26	34	79.1	272	21 <th>US-09-791-537-3472</th> <th>Sequence 3472, App</th>	US-09-791-537-3472	Sequence 3472, App
27	34	79.1	318	21 <th>US-09-791-537-111350</th> <th>Sequence 111350, A</th>	US-09-791-537-111350	Sequence 111350, A
28	34	79.1	323	21 <th>US-09-791-537-31968</th> <th>Sequence 31968, A</th>	US-09-791-537-31968	Sequence 31968, A
29	34	79.1	360	17 <th>US-09-340-684-3</th> <th>Sequence 3, App</th>	US-09-340-684-3	Sequence 3, App
30	34	79.1	374	21 <th>US-09-829-378-3</th> <th>Sequence 3, App</th>	US-09-829-378-3	Sequence 3, App
31	34	79.1	374	21 <th>US-09-791-537-24233</th> <th>Sequence 24233, A</th>	US-09-791-537-24233	Sequence 24233, A
32	34	79.1	379	21 <th>US-09-791-537-107991</th> <th>Sequence 107991, A</th>	US-09-791-537-107991	Sequence 107991, A
33	34	79.1	381	21 <th>US-09-791-537-73354</th> <th>Sequence 73354, A</th>	US-09-791-537-73354	Sequence 73354, A
34	34	79.1	388	21 <th>US-09-791-537-53837</th> <th>Sequence 53837, A</th>	US-09-791-537-53837	Sequence 53837, A
35	34	79.1	388	21 <th>US-09-791-537-31482</th> <th>Sequence 31482, A</th>	US-09-791-537-31482	Sequence 31482, A
36	34	79.1	388	21 <th>US-09-791-537-33589</th> <th>Sequence 33589, A</th>	US-09-791-537-33589	Sequence 33589, A
37	34	79.1	388	21 <th>US-09-791-537-33603</th> <th>Sequence 33603, A</th>	US-09-791-537-33603	Sequence 33603, A
38	34	79.1	388	21 <th>US-09-791-537-33606</th> <th>Sequence 33606, A</th>	US-09-791-537-33606	Sequence 33606, A
39	34	79.1	388	21 <th>US-09-791-537-54495</th> <th>Sequence 54495, A</th>	US-09-791-537-54495	Sequence 54495, A
40	34	79.1	388	22 <th>US-09-855-768-754</th> <th>Sequence 754, App</th>	US-09-855-768-754	Sequence 754, App
41	34	79.1	388	22 <th>US-09-855-768-755</th> <th>Sequence 755, App</th>	US-09-855-768-755	Sequence 755, App
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43	34	79.1	388	22 <th>US-09-855-768-759</th> <th>Sequence 759, App</th>	US-09-855-768-759	Sequence 759, App
44	34	79.1	388	22 <th>US-09-855-768-767</th> <th>Sequence 767, App</th>	US-09-855-768-767	Sequence 767, App
45	34	79.1	388	22 <th>US-09-855-768-768</th> <th>Sequence 768, App</th>	US-09-855-768-768	Sequence 768, App

ALIGNMENTS

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PCT-US02-00383-13
; Sequence 13: Application PC/TUS0200383
; GENERAL INFORMATION:
; APPLICANT: Zavazava, Nick
; APPLICANT: Dassau, Lior
; APPLICANT: Buchesbaum, Samuel
; APPLICANT: Barnea, Elion
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLE
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/23058
; CURRENT APPLICATION NUMBER: PCT/US02/00383
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 09/865,584
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 372
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
PCT-US02-00383-13
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; Sequence 44755, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44755
; LENGTH: 1080
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: DOMAIN
; LOCATION: (1030)..(1045)
; OTHER INFORMATION: CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE domain
; OTHER INFORMATION: Identified by EMATRIX, accession number PR00105B, p-value=2.800e-
PCT-US01-08631-44755
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Query Match          100.0%; Score 43; DB 1; Length 1080;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      315 GLEKNIEL 323
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; Sequence 2114, Application US/60389897
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boi D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Steven W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465P2
; CURRENT APPLICATION NUMBER: US/60/389,987
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2114
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-389-987-2114
```

```
Query Match          100.0%; Score 43; DB 27; Length 1280;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 GLEKNIEL 9
        |||||||
Db      89 GLEKNIEL 97
```

```
RESULT 8
US-60-412-418-2114
; Sequence 2114, Application US/60412418
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boi D.
```

```
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465P3
; CURRENT APPLICATION NUMBER: US/60/412,418
; CURRENT FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2114
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-412-418-2114
```

```
Query Match          100.0%; Score 43; DB 27; Length 1280;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 GLEKNIEL 9
        |||||||
Db      89 GLEKNIEL 97
```

```
RESULT 9
US-09-488-725A-3447
; Sequence 3447, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784F1PCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: PL_FL_genes_b Versions 1.0
; SEQ ID NO 3447
; LENGTH: 1604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3447
```

```
Query Match          100.0%; Score 43; DB 18; Length 1603;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 GLEKNIEL 9
        |||||||
Db      425 GLEKNIEL 433
```

```
RESULT 10
US-09-538-092-1016
; Sequence 1016, Application US/09538092
; GENERAL INFORMATION:
```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30279
; LENGTH: 269
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150-30279

```

```

Query Match      81.4%; Score 35; DB 20; Length 269;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 LIEKNIEL 9
        |||||:
Db      23 LIEKNIEL 30

```

```

RESULT 15
US-60-191-637-29827
; Sequence 29827, Application US/60191637
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
; FILE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
; FILE REFERENCE: CLO00392
; CURRENT APPLICATION NUMBER: US/60/191,637
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 4260
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29827
; LENGTH: 269
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-60-191-637-29827

```

```

Query Match      81.4%; Score 35; DB 27; Length 269;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 LIEKNIEL 9
        |||||:
Db      23 LIEKNIEL 30

```

Search completed: February 4, 2003, 17:41:25
Job time : 141 secs